

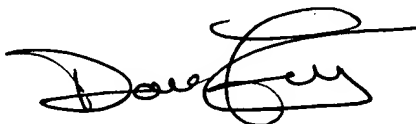
REMARKS

In response to the Notice of Defective Response, a copy of the substitute sequence listing in computer readable form is attached hereto. The content of the paper copy of the sequence listing and the copy of the sequence listing in computer readable form is the same, and includes no new matter.

It is believed that by submitting the present amendment and the sequence listing diskette, the application now fully complies with the requirements of 37 CFR §§ 1.821-1.825. Applicants respectfully solicit issuance of the patent.

Please charge any shortage in fees due in connection with the filing of this paper, including Extension of Time fees to Deposit Account No. 11-0345. Please credit any excess fees to such deposit account.

Respectfully submitted,  
KEIL & WEINKAUF



David C. Liechty  
Reg. No. 48,692

1101 Connecticut Ave., N.W.  
Washington, D.C. 20036  
(202)659-0100

DCL/kas

**BEST AVAILABLE COPY**

## SEQUENCE LISTING

<110> Kock, Michael  
 Hoeger, Thomas  
 Kroeger, Burkhard  
 Otterbach, Bernd  
 Lubisch, Wilfried  
 Lemaire, Hans-Georg

<120> Poly (ADP-ribose) polymerase-gene

<130> 0050/49100

<140> US 09/701,586

<141> 1999-06-04

<150> PCT/EP99/03889

<151> 1999-06-04

<160> 33

<170> PatentIn/WordPerfect

<210> 1

<211> 1843

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (3)...(1715)

<223> product is Poly ADP Ribose Polymerase; from brain tissue

<400> 1

cc atg gcg gcg cgg cgg cga cgg agc acc ggc ggc ggc agg gcg aga 47  
 Met Ala Ala Arg Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg  
 1 5 10 15

gca tta aat gaa agc aaa aga gtt aat aat ggc aac acg gct cca gaa 95  
 Ala Leu Asn Glu Ser Lys Arg Val Asn Asn Gly Asn Thr Ala Pro Glu  
 20 25 30

gac tct tcc cct gcc aag aaa act cgt aga tgc cag aga cag gag tcg 143  
 Asp Ser Ser Pro Ala Lys Lys Thr Arg Arg Cys Gln Arg Gln Glu Ser  
 35 40 45

aaa aag atg cct gtg gct gga gga aaa gct aat aag gac agg aca gaa 191  
 Lys Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp Arg Thr Glu  
 50 55 60

gac aag caa gat gaa tct gtg aag gcc ttg ctg tta aag ggc aaa gct 239  
 Asp Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Leu Lys Gly Lys Ala

BEST AVAILABLE COPY

65

70

75

cct gtg gac cca gag tgt aca gcc aag gtg ggg aag gct cat gtg tat 287  
 Pro Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr  
 80 85 90 95

tgt gaa gga aat gat gtc tat gat gtc atg cta aat cag acc aat ctc 335  
 Cys Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu  
 100 105 110

cag ttc aac aac aac aag tac tat ctg att cag cta tta gaa gat gat 383  
 Gln Phe Asn Asn Asn Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp  
 115 120 125

gcc cag agg aac ttc agt gtt tgg atg aga tgg ggc cga gtt ggg aaa 431  
 Ala Gln Arg Asn Phe Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys  
 130 135 140

atg gga cag cac agc ctg gtg gct tgt tca ggc aat ctc aac aag gcc 479  
 Met Gly Gln His Ser Leu Val Ala Cys Ser Gly Asn Leu Asn Lys Ala  
 145 150 155

aag gaa atc ttt cag aag aaa ttc ctt gac aaa acg aaa aac aat tgg 527  
 Lys Glu Ile Phe Gln Lys Lys Phe Leu Asp Lys Thr Lys Asn Asn Trp  
 160 165 170 175

gaa gat cga gaa aag ttt gag aag gtg cct gga aaa tat gat atg cta 575  
 Glu Asp Arg Glu Lys Phe Glu Lys Val Pro Gly Lys Tyr Asp Met Leu  
 180 185 190

cag atg gac tat gcc acc aat act cag gat gaa gag gaa aca aag aaa 623  
 Gln Met Asp Tyr Ala Thr Asn Thr Gln Asp Glu Glu Glu Thr Lys Lys  
 195 200 205

gag gaa tct ctt aaa tct ccc ttg aag cca gag tca cag cta gat ctt 671  
 Glu Glu Ser Leu Lys Ser Pro Leu Lys Pro Glu Ser Gln Leu Asp Leu  
 210 215 220

cgg gta cag gag tta ata aag ttg atc tgt aat gtt cag gcc atg gaa 719  
 Arg Val Gln Glu Leu Ile Lys Leu Ile Cys Asn Val Gln Ala Met Glu  
 225 230 235

gaa atg atg atg gaa atg aag tat aat acc aag aaa gcc cca ctt ggg 767  
 Glu Met Met Met Glu Met Lys Tyr Asn Thr Lys Lys Ala Pro Leu Gly  
 240 245 250 255

aag ctg aca gtg gca caa atc aag gca ggt tac cag tct ctt aag aag 815  
 Lys Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys  
 260 265 270

att gag gat tgt att cgg gct ggc cag cat gga cga gct ctc atg gaa 863  
 Ile Glu Asp Cys Ile Arg Ala Gly Gln His Gly Arg Ala Leu Met Glu  
 275 280 285

gca tgc aat gaa ttc tac acc agg att ccg cat gac ttt gga ctc cgt 911  
 Ala Cys Asn Glu Phe Tyr Thr Arg Ile Pro His Asp Phe Gly Leu Arg  
 290 295 300

act cct cca cta atc cgg aca cag aag gaa ctg tca gaa aaa ata caa 959  
 Thr Pro Pro Leu Ile Arg Thr Gln Lys Glu Leu Ser Glu Lys Ile Gln  
 305 310 315

tta cta gag gct ttg gga gac att gaa att gct att aag ctg gtg aaa 1007  
 Leu Leu Glu Ala Leu Gly Asp Ile Glu Ile Ala Ile Lys Leu Val Lys  
 320 325 330 335

aca gag cta caa agc cca gaa cac cca ttg gac caa cac tat aga aac 1055  
 Thr Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg Asn  
 340 345 350

cta cat tgt gcc ttg cgc ccc ctt gac cat gaa agt tac gag ttc aaa 1103  
 Leu His Cys Ala Leu Arg Pro Leu Asp His Glu Ser Tyr Glu Phe Lys  
 355 360 365

gtg att tcc cag tac cta caa tct acc cat gct ccc aca cac agc gac 1151  
 Val Ile Ser Gln Tyr Leu Gln Ser Thr His Ala Pro Thr His Ser Asp  
 370 375 380

tat acc atg acc ttg ctg gat ttg ttt gaa gtg gag aag gat ggt gag 1199  
 Tyr Thr Met Thr Leu Leu Asp Leu Phe Glu Val Glu Lys Asp Gly Glu  
 385 390 395

aaa gaa gcc ttc aga gag gac ctt cat aac agg atg ctt cta tgg cat 1247  
 Lys Glu Ala Phe Arg Glu Asp Leu His Asn Arg Met Leu Leu Trp His  
 400 405 410 415

ggt tcc agg atg agt aac tgg gtg gga atc ttg agc cat ggg ctt cga 1295  
 Gly Ser Arg Met Ser Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg  
 420 425 430

att gcc cca cct gaa gct ccc atc aca ggt tac atg ttt ggg aaa gga 1343  
 Ile Ala Pro Pro Glu Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly  
 435 440 445

atc tac ttt gct gac atg tct tcc aag agt gcc aat tac tgc ttt gcc 1391  
 Ile Tyr Phe Ala Asp Met Ser Ser Lys Ser Ala Asn Tyr Cys Phe Ala  
 450 455 460

tct cgc cta aag aat aca gga ctg ctg ctc tta tca gag gta gct cta 1439  
 Ser Arg Leu Lys Asn Thr Gly Leu Leu Leu Leu Ser Glu Val Ala Leu  
 465 470 475

ggt cag tgt aat gaa cta cta gag gcc aat cct aag gcc gaa gga ttg 1487  
 Gly Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu  
 480 485 490 495

ctt caa ggt aaa cat agc acc aag ggg ctg ggc aag atg gct ccc agt 1535

Leu	Gln	Gly	Lys	His	Ser	Thr	Lys	Gly	Leu	Gly	Lys	Met	Ala	Pro	Ser		
				500					505					510			
tct	gcc	cac	ttc	gtc	acc	ctg	aat	ggg	agt	aca	gtg	cca	tta	gga	cca		1583
Ser	Ala	His	Phe	Val	Thr	Leu	Asn	Gly	Ser	Thr	Val	Pro	Leu	Gly	Pro		
			515					520					525				
gca	agt	gac	aca	gga	att	ctg	aat	cca	gat	ggg	tat	acc	ctc	aac	tac		1631
Ala	Ser	Asp	Thr	Gly	Ile	Leu	Asn	Pro	Asp	Gly	Tyr	Thr	Leu	Asn	Tyr		
			530				535					540					
aat	gaa	tat	att	gta	tat	aac	ccc	aac	cag	gtc	cgt	atg	cgg	tac	ctt		1679
Asn	Glu	Tyr	Ile	Val	Tyr	Asn	Pro	Asn	Gln	Val	Arg	Met	Arg	Tyr	Leu		
			545			550				555							
tta	aag	gtt	cag	ttt	aat	ttc	ctt	cag	ctg	tgg	tga	atgttgat					1725
Leu	Lys	Val	Gln	Phe	Asn	Phe	Leu	Gln	Leu	Trp							
560					565				570								

---

taaataaacc	agagatctga	tcttcaagca	agaaaataag	cagtgttgta	cttgtgaatt		1785
------------	------------	------------	------------	------------	------------	--	------

ttgtgatatt	ttatgtaata	aaaactgtac	aggtctaaaa	aaaaaaaaaa	aaaaaaaaaa		1843
------------	------------	------------	------------	------------	------------	--	------

&lt;210&gt; 2

&lt;211&gt; 570

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

Met	Ala	Ala	Arg	Arg	Arg	Arg	Ser	Thr	Gly	Gly	Gly	Arg	Ala	Arg	Ala		
1				5					10				15				

Leu	Asn	Glu	Ser	Lys	Arg	Val	Asn	Asn	Gly	Asn	Thr	Ala	Pro	Glu	Asp		
			20					25					30				

Ser	Ser	Pro	Ala	Lys	Lys	Thr	Arg	Arg	Cys	Gln	Arg	Gln	Glu	Ser	Lys		
		35				40					45						

Lys	Met	Pro	Val	Ala	Gly	Gly	Lys	Ala	Asn	Lys	Asp	Arg	Thr	Glu	Asp		
	50					55					60						

Lys	Gln	Asp	Glu	Ser	Val	Lys	Ala	Leu	Leu	Leu	Lys	Gly	Lys	Ala	Pro		
65					70				75						80		

---

Val	Asp	Pro	Glu	Cys	Thr	Ala	Lys	Val	Gly	Lys	Ala	His	Val	Tyr	Cys		
				85					90					95			

Glu	Gly	Asn	Asp	Val	Tyr	Asp	Val	Met	Leu	Asn	Gln	Thr	Asn	L	u	Gln	
		100						105					110				

Phe	Asn	Asn	Asn	Lys	Tyr	Tyr	Leu	Ile	Gln	Leu	Leu	Glu	Asp	Asp	Ala		
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--	--

115	120	125
Gln Arg Asn Phe Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys Met		
130	135	140
Gly Gln His Ser Leu Val Ala Cys Ser Gly Asn Leu Asn Lys Ala Lys		
145	150	155
Glu Ile Phe Gln Lys Lys Phe Leu Asp Lys Thr Lys Asn Asn Trp Glu		
165	170	175
Asp Arg Glu Lys Phe Glu Lys Val Pro Gly Lys Tyr Asp Met Leu Gln		
180	185	190
Met Asp Tyr Ala Thr Asn Thr Gln Asp Glu Glu Glu Thr Lys Lys Glu		
195	200	205
Glu Ser Leu Lys Ser Pro Leu Lys Pro Glu Ser Gln Leu Asp Leu Arg		
210	215	220
Val Gln Glu Leu Ile Lys Leu Ile Cys Asn Val Gln Ala Met Glu Glu		
225	230	235
Met Met Met Glu Met Lys Tyr Asn Thr Lys Lys Ala Pro Leu Gly Lys		
245	250	255
Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys Ile		
260	265	270
Glu Asp Cys Ile Arg Ala Gly Gln His Gly Arg Ala Leu Met Glu Ala		
275	280	285
Cys Asn Glu Phe Tyr Thr Arg Ile Pro His Asp Phe Gly Leu Arg Thr		
290	295	300
Pro Pro Leu Ile Arg Thr Gln Lys Glu Leu Ser Glu Lys Ile Gln Leu		
305	310	315
Leu Glu Ala Leu Gly Asp Ile Glu Ile Ala Ile Lys Leu Val Lys Thr		
325	330	335
Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg Asn Leu		
340	345	350
His Cys Ala Leu Arg Pro Leu Asp His Glu Ser Tyr Glu Phe Lys Val		
355	360	365
Ile Ser Gln Tyr Leu Gln Ser Thr His Ala Pro Thr His Ser Asp Tyr		
370	375	380
Thr Met Thr Leu Leu Asp Leu Phe Glu Val Glu Lys Asp Gly Glu Lys		
385	390	395
		400

Glu Ala Phe Arg Glu Asp Leu His Asn Arg Met Leu Leu Trp His Gly  
                             405                            410                            415

Ser Arg Met Ser Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg Ile  
                             420                            425                            430

Ala Pro Pro Glu Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly Ile  
                             435                            440                            445

Tyr Phe Ala Asp Met Ser Ser Lys Ser Ala Asn Tyr Cys Phe Ala Ser  
                             450                            455                            460

Arg Leu Lys Asn Thr Gly Leu Leu Leu Leu Ser Glu Val Ala Leu Gly  
                             465                            470                            475                            480

Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu Leu  
                             485                            490                            495

~~Gln Gly Lys His Ser Thr Lys Gly Leu Gly Lys Met Ala Pro Ser Ser~~  
                             500                            505                            510

Ala His Phe Val Thr Leu Asn Gly Ser Thr Val Pro Leu Gly Pro Ala  
                             515                            520                            525

Ser Asp Thr Gly Ile Leu Asn Pro Asp Gly Tyr Thr Leu Asn Tyr Asn  
                             530                            535                            540

Glu Tyr Ile Val Tyr Asn Pro Asn Gln Val Arg Met Arg Tyr Leu Leu  
                             545                            550                            555                            560

Lys Val Gln Phe Asn Phe Leu Gln Leu Trp  
                             565                            570

<210> 3

<211> 2265

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (242)...(1843)

<223> product is Poly ADP Ribose Polymerase; from uterus tissue

<400> 3

---

tgggactggt cgctgactc ggctgcccc agcctctgct tcacccact ggtggccaaa	60
tagccgatgt ctaatcccc acacaagctc atccccggcc tctgggattg ttgggaattc	120
tctccctaatt tcacgcctga ggctcatgga gagttgctag acctgggact gccctgggag	180
gcgcacacaa ccaggccggg tggcagccag gacctctccc atgtccctgc ttttcttggc	240

c atg gct cca aag ccg aag ccc tgg gta cag act gag ggc cct gag	286
Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro Glu	
1 5 10 15	
aag aag aag ggc cgg cag gca gga agg gag gag gac ccc ttc cgc tcc	334
Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser	
20 25 30	
acc gct gag gcc ctc aag gcc ata ccc gca gag aag cgc ata atc cgc	382
Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile Arg	
35 40 45	
gtg gat cca aca tgt cca ctc agc agc aac ccc ggg acc cag gtg tat	430
Val Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val Tyr	
50 55 60	
gag gac tac aac tgc acc ctg aac cag acc aac atc gag aac aac aac	478
Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn Asn	
65 70 75	
aac aag ttc tac atc atc cag ctg ctc caa gac agc aac cgc ttc ttc	526
Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe Phe	
80 85 90 95	
acc tgc tgg aac cgc tgg ggc cgt gtg gga gag gtc ggc cag tca aag	574
Thr Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys	
100 105 110	
atc aac cac ttc aca agg cta gaa gat gca aag aag gac ttt gag aag	622
Ile Asn His Phe Thr Arg Leu Glu Asp Ala Lys Lys Asp Phe Glu Lys	
115 120 125	
aaa ttt cgg gaa aag acc aag aac aac tgg gca gag cgg gac cac ttt	670
Lys Phe Arg Glu Lys Thr Lys Asn Asn Trp Ala Glu Arg Asp His Phe	
130 135 140	
gtg tct cac ccg ggc aag tac aca ctt atc gaa gta cag gca gag gat	718
Val Ser His Pro Gly Lys Tyr Thr Leu Ile Glu Val Gln Ala Glu Asp	
145 150 155	
gag gcc cag gaa gct gtg gtg aag gtg gac aga ggc cca gtg agg act	766
Glu Ala Gln Glu Ala Val Val Lys Val Asp Arg Gly Pro Val Arg Thr	
160 165 170 175	
gtg act aag ccg gtg cag ccc tgc tcc ctg gac cca gcc acg cag aag	814
Val Thr Lys Arg Val Gln Pro Cys Ser Leu Asp Pro Ala Thr Gln Lys	
180 185 190	
ctc atc act aac atc ttc agc aag gag atg ttc aag aac acc atg gcc	862
Leu Ile Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Thr Met Ala	
195 200 205	
ctc atg gac ctg gat gtg aag aag atg ccc ctg gga aag ctg agc aag	910



Leu	Met	Asp	Leu	Asp	Val	Lys	Lys	Met	Pro	Leu	Gly	Lys	Leu	Ser	Lys		
	210						215					220					
caa	cag	att	gca	cgg	ggt	ttc	gag	gcc	ttg	gag	gcg	ctg	gag	gag	gcc		958
Gln	Gln	Ile	Ala	Arg	Gly	Phe	Glu	Ala	Leu	Glu	Ala	Leu	Glu	Glu	Ala		
	225					230					235						
ctg	aaa	ggc	ccc	acg	gat	ggt	ggc	caa	agc	ctg	gag	gag	ctg	tcc	tca		1006
Leu	Lys	Gly	Pro	Thr	Asp	Gly	Gly	Gln	Ser	Leu	Glu	Glu	Leu	Ser	Ser		
	240				245				250					255			
cac	ttt	tac	acc	gtc	atc	ccg	cac	aac	ttc	ggc	cac	agc	cag	ccc	ccg		1054
His	Phe	Tyr	Thr	Val	Ile	Pro	His	Asn	Phe	Gly	His	Ser	Gln	Pro	Pro		
				260				265						270			
ccc	atc	aat	tcc	cct	gag	ctt	ctg	cag	gcc	aag	aag	gac	atg	ctg	ctg		1102
Pro	Ile	Asn	Ser	Pro	Glu	Leu	Leu	Gln	Ala	Lys	Lys	Asp	Met	Leu	Leu		
			275					280					285				
gtg	ctg	gcg	gac	atc	gag	ctg	gcc	cag	gcc	ctg	cag	gca	gtc	tct	gag		1150
Val	Leu	Ala	Asp	Ile	Glu	Leu	Ala	Gln	Ala	Leu	Gln	Ala	Val	Ser	Glu		
		290					295					300					
cag	gag	aag	acg	gtg	gag	gag	gtg	cca	cac	ccc	ctg	gac	cga	gac	tac		1198
Gln	Glu	Lys	Thr	Val	Glu	Glu	Val	Pro	His	Pro	Leu	Asp	Arg	Asp	Tyr		
	305					310					315						
cag	ctt	ctc	aag	tgc	cag	ctg	cag	ctg	cta	gac	tct	gga	gca	cct	gag		1246
Gln	Leu	Leu	Lys	Cys	Gln	Leu	Gln	Leu	Leu	Asp	Ser	Gly	Ala	Pro	Glu		
	320				325					330				335			
tac	aag	gtg	ata	cag	acc	tac	tta	gaa	cag	act	ggc	agc	aac	cac	agg		1294
Tyr	Lys	Val	Ile	Gln	Thr	Tyr	Leu	Glu	Gln	Thr	Gly	Ser	Asn	His	Arg		
				340					345					350			
tgc	cct	aca	ctt	caa	cac	atc	tgg	aaa	gta	aac	caa	gaa	ggg	gag	gaa		1342
Cys	Pro	Thr	Leu	Gln	His	Ile	Trp	Lys	Val	Asn	Gln	Glu	Gly	Glu	Glu		
			355					360					365				
gac	aga	ttc	cag	gcc	cac	tcc	aaa	ctg	ggt	aat	cgg	aag	ctg	ctg	tgg		1390
Asp	Arg	Phe	Gln	Ala	His	Ser	Lys	Leu	Gly	Asn	Arg	Lys	Leu	Leu	Trp		
		370					375					380					
cat	ggc	acc	aac	atg	gcc	gtg	gtg	gcc	gcc	atc	ctc	act	agt	ggg	ctc		1438
His	Gly	Thr	Asn	Met	Ala	Val	Val	Ala	Ala	Ile	Leu	Thr	Ser	Gly	Leu		
	385					390					395						
cgc	atc	atg	cca	cat	tct	ggt	ggg	cgt	ggt	ggc	aag	ggc	atc	tac	ttt		1486
Arg	Ile	Met	Pro	His	Ser	Gly	Gly	Arg	Val	Gly	Lys	Gly	Ile	Tyr	Phe		
	400				405					410				415			
gcc	tca	gag	aac	agc	aag	tca	gct	gga	tat	ggt	att	ggc	atg	aag	tgt		1534
Ala	Ser	Glu	Asn	Ser	Lys	Ser	Ala	Gly	Tyr	Val	Ile	Gly	Met	Lys	Cys		

420	425	430	
ggg gcc cac cat gtc ggc tac atg ttc ctg ggt gag gtg gcc ctg ggc			1582
Gly Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly			
435	440	445	
aga gag cac cat atc aac acg gac aac ccc agc ttg aag agc cca cct			1630
Arg Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro Pro			
450	455	460	
cct ggc ttc gac agt gtc att gcc cga ggc cac acc gag cct gat ccg			1678
Pro Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp Pro			
465	470	475	
acc cag gac act gag ttg gag ctg gat ggc cag caa gtg gtg gtg ccc			1726
Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val Pro			
480	485	490	495
cag ggc cag cct gtg ccc tgc cca gag ttc agc agc tcc aca ttc tcc			1774
Gln Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe Ser			
500	505	510	
cag agc gag tac ctc atc tac cag gag agc cag tgt cgc ctg cgc tac			1822
Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg Tyr			
515	520	525	
ctg ctg gag gtc cac ctc tga gtgccccgcc tgcccccggt ggtcctgcaa			1873
Leu Leu Glu Val His Leu			
530			
ggctggactg tgatcttcaa tcatectgcc catctctggt acccctatat cactcctttt			1933
tttcaagaat acaatacggtt gttgttaact atagtcacca tgctgtacaa gatccctgaa			1993
cttatgcctc ctaactgaaa ttttgtattc tttgacacat ctgcccagtc cctctcctcc			2053
cagcccatgg taaccagcat ttgactcttt acttgtataa gggcagcttt tataggttcc			2113
acatgtaagt gagatcatgc agtgtttgtc tttctgtgcc tggcttattt cactcagcat			2173
aatgtgcacc gggttcaccc atgttttcat aaatgacaag atttcctcct ttaaaaaaaaa			2233
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa			2265

---

<210> 4

<211> 533

<212> PRT

<213> Homo sapiens

<400> 4

Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro Glu Lys

1	5	10	15
Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser Thr	20	25	30
Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile Arg Val	35	40	45
Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val Tyr Glu	50	55	60
Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn Asn Asn	65	70	75
Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe Phe Thr	85	90	95
Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Ile	100	105	110
Asn His Phe Thr Arg Leu Glu Asp Ala Lys Lys Asp Phe Glu Lys Lys	115	120	125
Phe Arg Glu Lys Thr Lys Asn Asn Trp Ala Glu Arg Asp His Phe Val	130	135	140
Ser His Pro Gly Lys Tyr Thr Leu Ile Glu Val Gln Ala Glu Asp Glu	145	150	155
Ala Gln Glu Ala Val Val Lys Val Asp Arg Gly Pro Val Arg Thr Val	165	170	175
Thr Lys Arg Val Gln Pro Cys Ser Leu Asp Pro Ala Thr Gln Lys Leu	180	185	190
Ile Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Thr Met Ala Leu	195	200	205
Met Asp Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Ser Lys Gln	210	215	220
Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Leu	225	230	235
Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser Ser His	245	250	255
Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro Pro Pro	260	265	270
Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu Leu Val	275	280	285

Leu Ala Asp Ile Glu Leu Ala Gln Ala Leu Gln Ala Val Ser Glu Gln  
 290 295 300

Glu Lys Thr Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln  
 305 310 315 320

Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro Glu Tyr  
 325 330 335

Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His Arg Cys  
 340 345 350

Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu Glu Asp  
 355 360 365

Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu Trp His  
 370 375 380

~~Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg~~  
 385 390 395 400

Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala  
 405 410 415

Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys Cys Gly  
 420 425 430

Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Arg  
 435 440 445

Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro Pro Pro  
 450 455 460

Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp Pro Thr  
 465 470 475 480

Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val Pro Gln  
 485 490 495

Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe Ser Gln  
 500 505 510

Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg Tyr Leu  
 515 520 525

~~Leu Glu Val His Leu~~  
 530

<210> 5

<211> 2265

<212> DNA

<213> Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (221)...(1843)

&lt;223&gt; product is Poly ADP Ribose Polymerase; from uterus tissue

&lt;400&gt; 5

tgggactggt cgctgactc ggctgcccc agcctctgct tcacccact ggtggccaaa 60

tagccgatgt ctaatcccc acacaagctc atccccggcc tctgggattg ttgggaattc 120

tctccctaatt tcacgcctga ggctcatgga gagttgctag acctgggact gccctgggag 180

gcgcacacaa ccaggccggg tggcagccag gacctctccc atg tcc ctg ctt ttc 235  
Met Ser Leu Leu Phe  
1 5

ttg gcc atg gct cca aag ccg aag ccc tgg gta cag act gag ggc cct 283  
Leu Ala Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro  
10 15 20

gag aag aag aag ggc cgg cag gca gga agg gag gag gac ccc ttc cgc 331  
Glu Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg  
25 30 35

tcc acc gct gag gcc ctc aag gcc ata ccc gca gag aag cgc ata atc 379  
Ser Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile  
40 45 50

cgc gtg gat cca aca tgt cca ctc agc agc aac ccc ggg acc cag gtg 427  
Arg Val Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val  
55 60 65

tat gag gac tac aac tgc acc ctg aac cag acc aac atc gag aac aac 475  
Tyr Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn  
70 75 80 85

aac aac aag ttc tac atc atc cag ctg ctc caa gac agc aac cgc ttc 523  
Asn Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe  
90 95 100

ttc acc tgc tgg aac cgc tgg ggc cgt gtg gga gag gtc ggc cag tca 571  
Phe Thr Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser  
105 110 115

aag atc aac cac ttc aca agg cta gaa gat gca aag aag gac ttt gag 619  
Lys Ile Asn His Phe Thr Arg Leu Glu Asp Ala Lys Lys Asp Phe Glu  
120 125 130

aag aaa ttt cgg gaa aag acc aag aac aac tgg gca gag cgg gac cac 667  
Lys Lys Phe Arg Glu Lys Thr Lys Asn Asn Trp Ala Glu Arg Asp His  
135 140 145

ttt gtg tct cac ccg ggc aag tac aca ctt atc gaa gta cag gca gag Phe Val Ser His Pro Gly Lys Tyr Thr Leu Ile Glu Val Gln Ala Glu 150 155 160 165	715
gat gag gcc cag gaa gct gtg gtg aag gtg gac aga ggc cca gtg agg Asp Glu Ala Gln Glu Ala Val Val Lys Val Asp Arg Gly Pro Val Arg 170 175 180	763
act gtg act aag cgg gtg cag ccc tgc tcc ctg gac cca gcc acg cag Thr Val Thr Lys Arg Val Gln Pro Cys Ser Leu Asp Pro Ala Thr Gln 185 190 195	811
aag ctc atc act aac atc ttc agc aag gag atg ttc aag aac acc atg Lys Leu Ile Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Thr Met 200 205 210	859
gcc ctc atg gac ctg gat gtg aag aag atg ccc ctg gga aag ctg agc Ala Leu Met Asp Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Ser 215 220 225	907
aag caa cag att gca cgg ggt ttc gag gcc ttg gag gcg ctg gag gag Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu 230 235 240 245	955
gcc ctg aaa ggc ccc acg gat ggt ggc caa agc ctg gag gag ctg tcc Ala Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser 250 255 260	1003
tca cac ttt tac acc gtc atc ccg cac aac ttc ggc cac agc cag ccc Ser His Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro 265 270 275	1051
ccg ccc atc aat tcc cct gag ctt ctg cag gcc aag aag gac atg ctg Pro Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu 280 285 290	1099
ctg gtg ctg gcg gac atc gag ctg gcc cag gcc ctg cag gca gtc tct Leu Val Leu Ala Asp Ile Glu Leu Ala Gln Ala Leu Gln Ala Val Ser 295 300 305	1147
gag cag gag aag acg gtg gag gag gtg cca cac ccc ctg gac cga gac Glu Gln Glu Lys Thr Val Glu Glu Val Pro His Pro Leu Asp Arg Asp 310 315 320 325	1195
tac cag ctt ctc aag tgc cag ctg cag ctg cta gac tct gga gca cct Tyr Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro 330 335 340	1243
gag tac aag gtg ata cag acc tac tta gaa cag act ggc agc aac cac Glu Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His 345 350 355	1291
agg tgc cct aca ctt caa cac atc tgg aaa gta aac caa gaa ggg gag	1339

[illegible]

```

cagcccatgg taaccagcat ttgactcttt acttgataaa gggcagcttt tataggttcc 2113
acatgtaagt gagatcatgc agtggtttgtc tttctgtgcc tggcttattt cactcagcat 2173
aatgtgcacc gggttcaccc atgttttcat aaatgacaag atttcctcct ttaaaaaaaaa 2233
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 2265

```

```

<210> 6
<211> 540
<212> PRT
<213> Homo sapiens

```

```

<400> 6

```

```

Met Ser Leu Leu Phe Leu Ala Met Ala Pro Lys Pro Lys Pro Trp Val
  1             5             10             15

```

```

Gln Thr Glu Gly Pro Glu Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu
      20             25             30

```

```

Glu Asp Pro Phe Arg Ser Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala
      35             40             45

```

```

Glu Lys Arg Ile Ile Arg Val Asp Pro Thr Cys Pro Leu Ser Ser Asn
      50             55             60

```

```

Pro Gly Thr Gln Val Tyr Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr
      65             70             75             80

```

```

Asn Ile Glu Asn Asn Asn Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln
      85             90             95

```

```

Asp Ser Asn Arg Phe Phe Thr Cys Trp Asn Arg Trp Gly Arg Val Gly
     100             105             110

```

```

Glu Val Gly Gln Ser Lys Ile Asn His Phe Thr Arg Leu Glu Asp Ala
     115             120             125

```

```

Lys Lys Asp Phe Glu Lys Lys Phe Arg Glu Lys Thr Lys Asn Asn Trp
     130             135             140

```

```

Ala Glu Arg Asp His Phe Val Ser His Pro Gly Lys Tyr Thr Leu Ile
     145             150             155             160

```

```

Glu Val Gln Ala Glu Asp Glu Ala Gln Glu Ala Val Val Lys Val Asp
     165             170             175

```

```

Arg Gly Pro Val Arg Thr Val Thr Lys Arg Val Gln Pro Cys Ser Leu
     180             185             190

```

```

Asp Pro Ala Thr Gln Lys Leu Ile Thr Asn Ile Phe Ser Lys Glu Met

```



195	200	205
Phe Lys Asn Thr Met Ala Leu Met Asp Leu Asp Val Lys Lys Met Pro 210 215 220		
Leu Gly Lys Leu Ser Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu 225 230 235 240		
Glu Ala Leu Glu Glu Ala Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser 245 250 255		
Leu Glu Glu Leu Ser Ser His Phe Tyr Thr Val Ile Pro His Asn Phe 260 265 270		
Gly His Ser Gln Pro Pro Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala 275 280 285		
Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu Ala Gln Ala 290 295 300		
Leu Gln Ala Val Ser Glu Gln Glu Lys Thr Val Glu Glu Val Pro His 305 310 315 320		
Pro Leu Asp Arg Asp Tyr Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu 325 330 335		
Asp Ser Gly Ala Pro Glu Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln 340 345 350		
Thr Gly Ser Asn His Arg Cys Pro Thr Leu Gln His Ile Trp Lys Val 355 360 365		
Asn Gln Glu Gly Glu Glu Asp Arg Phe Gln Ala His Ser Lys Leu Gly 370 375 380		
Asn Arg Lys Leu Leu Trp His Gly Thr Asn Met Ala Val Val Ala Ala 385 390 395 400		
Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser Gly Gly Arg Val 405 410 415		
Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr 420 425 430		
Val Ile Gly Met Lys Cys Gly Ala His His Val Gly Tyr Met Phe Leu 435 440 445		
Gly Glu Val Ala Leu Gly Arg Glu His His Ile Asn Thr Asp Asn Pro 450 455 460		
Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val Ile Ala Arg Gly 465 470 475 480		

His	Thr	Glu	Pro	Asp	Pro	Thr	Gln	Asp	Thr	Glu	Leu	Glu	Leu	Asp	Gly
				485					490					495	
Gln	Gln	Val	Val	Val	Pro	Gln	Gly	Gln	Pro	Val	Pro	Cys	Pro	Glu	Phe
			500					505					510		
Ser	Ser	Ser	Thr	Phe	Ser	Gln	Ser	Glu	Tyr	Leu	Ile	Tyr	Gln	Glu	Ser
		515					520					525			
Gln	Cys	Arg	Leu	Arg	Tyr	Leu	Leu	Glu	Val	His	Leu				
	530					535					540				

```
<210> 7
<211> 1740
<212> DNA
<213> Mus musculus
```

```
<220>  
<221> CDS  
<222> (112)...(1710)
```

<400> 7

cccggttttc acttttctg ctgcctcggg gaacacctcg agccaactgc ttcctaactc      60

agggtgggca gaactgacgg gatctaagct tctgcatctc tgaggagaac c atg gct      117  
Met Ala  
1

cca aaa cga aag gcc tct gtg cag act gag ggc tcc aag aag cag cga 165  
Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys Gln Arg  
5 10 15

caa ggg aca gag gag gag gac agc ttc cgg tcc act gcc gag gct ctc 213  
Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu Ala Leu  
20 25 30

aga gca gca cct gct gat aat cgg gtc atc cgt gtg gac ccc tca tgt 261  
Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro Ser Cys  
35 40 45 50

cca ttc agc cgg aac ccc ggg ata cag gtc cac gag gac tat gac tgt 309  
Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr Asp Cys  
55 60 65

acc ctg aac cag acc aac atc ggc aac aac aac aac aag ttc tat att 357  
Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe Tyr Ile  
70 75 80

atc caa ctg ctg gag gag ggt agt cgc ttc ttc tgc tgg aat cgc tgg 405  
Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn Arg Trp  
85 90 95

ggc cgc gtg gga gag gtg ggc cag agc aag atg aac cac ttc acc tgc	453
Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe Thr Cys	
100 105 110	
ctg gaa gat gca aag aag gac ttt aag aag aaa ttt tgg gag aag act	501
Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu Lys Thr	
115 120 125 130	
aaa aac aaa tgg gag gag cgg gac cgt ttt gtg gcc cag ccc aac aag	549
Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro Asn Lys	
135 140 145	
tac aca ctt ata gaa gtc cag gga gaa gca gag agc caa gag gct gta	597
Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu Ala Val	
150 155 160	
gtg aag gcc tta tct ccc cag gtg gac agc ggc cct gtg agg acc gtg	645
Val Lys Ala Leu Ser Pro Gln Val Asp Ser Gly Pro Val Arg Thr Val	
165 170 175	
gtc aag ccc tgc tcc cta gac cct gcc acc cag aac ctt atc acc aac	693
Val Lys Pro Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn	
180 185 190	
atc ttc agc aaa gag atg ttc aag aac gca atg acc ctc atg aac ctg	741
Ile Phe Ser Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu	
195 200 205 210	
gat gtg aag aag atg ccc ttg gga aag ctg acc aag cag cag att gcc	789
Asp Val Lys Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala	
215 220 225	
cgt ggc ttc gag gcc ttg gaa gct cta gag gag gcc atg aaa aac ccc	837
Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro	
230 235 240	
aca ggg gat ggc cag agc ctg gaa gag ctc tcc tcc tgc ttc tac act	885
Thr Gly Asp Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr	
245 250 255	
gtc atc cca cac aac ttc ggc cgc agc cga ccc ccg ccc atc aac tcc	933
Val Ile Pro His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser	
260 265 270	
cct gat gtg ctt cag gcc aag aag gac atg ctg ctg gtg cta gcg gac	981
Pro Asp Val Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp	
275 280 285 290	
atc gag ttg gcg cag acc ttg cag gca gcc cct ggg gag gag gag gag	1029
Il Glu Leu Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Glu	
295 300 305	
aaa gtg gaa gag gtg cca cac cca ctg gat cga gac tac cag ctc ctc	1077

Lys	Val	Glu	Glu	Val	Pro	His	Pro	Leu	Asp	Arg	Asp	Tyr	Gln	Leu	Leu	
		310						315					320			
agg	tgc	cag	ctt	caa	ctg	ctg	gac	tcc	ggg	gag	tcc	gag	tac	aag	gca	1125
Arg	Cys	Gln	Leu	Gln	Leu	Leu	Asp	Ser	Gly	Glu	Ser	Glu	Tyr	Lys	Ala	
		325					330					335				
ata	cag	acc	tac	ctg	aaa	cag	act	ggc	aac	agc	tac	agg	tgc	cca	aac	1173
Ile	Gln	Thr	Tyr	Leu	Lys	Gln	Thr	Gly	Asn	Ser	Tyr	Arg	Cys	Pro	Asn	
		340				345					350					
ctg	cgg	cat	gtt	tgg	aaa	gtg	aac	cga	gaa	ggg	gag	gga	gac	agg	ttc	1221
Leu	Arg	His	Val	Trp	Lys	Val	Asn	Arg	Glu	Gly	Glu	Gly	Asp	Arg	Phe	
	355				360				365						370	
cag	gcc	cac	tcc	aaa	ctg	ggc	aat	cgg	agg	ctg	ctg	tgg	cac	ggc	acc	1269
Gln	Ala	His	Ser	Lys	Leu	Gly	Asn	Arg	Arg	Leu	Leu	Trp	His	Gly	Thr	
				375				380						385		
aat	gtg	gcc	gtg	gtg	gct	gcc	atc	ctc	acc	agt	ggg	ctc	cga	atc	atg	1317
Asn	Val	Ala	Val	Val	Ala	Ala	Ile	Leu	Thr	Ser	Gly	Leu	Arg	Ile	Met	
			390					395					400			
cca	cac	tcg	ggt	ggt	cgt	gtt	ggc	aag	ggt	att	tat	ttt	gcc	tct	gag	1365
Pro	His	Ser	Gly	Gly	Arg	Val	Gly	Lys	Gly	Ile	Tyr	Phe	Ala	Ser	Glu	
		405					410					415				
aac	agc	aag	tca	gct	ggc	tat	gtt	acc	acc	atg	cac	tgt	ggg	ggc	cac	1413
Asn	Ser	Lys	Ser	Ala	Gly	Tyr	Val	Thr	Thr	Met	His	Cys	Gly	Gly	His	
	420					425					430					
cag	gtg	ggc	tac	atg	ttc	ctg	ggc	gag	gtg	gcc	ctc	ggc	aaa	gag	cac	1461
Gln	Val	Gly	Tyr	Met	Phe	Leu	Gly	Glu	Val	Ala	Leu	Gly	Lys	Glu	His	
	435				440					445				450		
cac	atc	acc	atc	gat	gac	ccc	agc	ttg	aag	agt	cca	ccc	cct	ggc	ttt	1509
His	Ile	Thr	Ile	Asp	Asp	Pro	Ser	Leu	Lys	Ser	Pro	Pro	Pro	Gly	Phe	
				455				460						465		
gac	agc	gtc	atc	gcc	cga	ggc	caa	acc	gag	cgc	gat	ccc	gcc	cag	gac	1557
Asp	Ser	Val	Ile	Ala	Arg	Gly	Gln	Thr	Glu	Pro	Asp	Pro	Ala	Gln	Asp	
			470					475					480			
att	gaa	ctt	gaa	ctg	gat	ggg	cag	cgc	gtg	gtg	gtg	ccc	caa	ggc	cgc	1605
Ile	Glu	Leu	Glu	Leu	Asp	Gly	Gln	Pro	Val	Val	Val	Pro	Gln	Gly	Pro	
		485					490					495				
cct	gtg	cag	tgc	cgc	tca	ttc	aaa	agc	tcc	agc	ttc	agc	cag	agt	gaa	1653
Pro	Val	Gln	Cys	Pro	Ser	Phe	Lys	Ser	Ser	Ser	Phe	Ser	Gln	Ser	Glu	
		500				505					510					
tac	ctc	ata	tac	aag	gag	agc	cag	tgt	cgc	ctg	cgc	tac	ctg	ctg	gag	1701
Tyr	Leu	Ile	Tyr	Lys	Glu	Ser	Gln	Cys	Arg	Leu	Arg	Tyr	Leu	Leu	Glu	

515

520

525

530

att cac ctc taagctgctt gccctcccta ggtccaagcc  
 ile His Leu

1740

&lt;210&gt; 8

&lt;211&gt; 533

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 8

Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys  
 1 5 10 15

Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu  
 20 25 30

Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro  
 35 40 45

Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr  
 50 55 60

Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe  
 65 70 75 80

Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn  
 85 90 95

Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe  
 100 105 110

Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu  
 115 120 125

Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro  
 130 135 140

Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu  
 145 150 155 160

Ala Val Val Lys Ala Leu Ser Pro Gln Val Asp Ser Gly Pro Val Arg  
 165 170 175

Thr Val Val Lys Pro Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile  
 180 185 190

Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met  
 195 200 205

Asn Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln

210	215	220
Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys 225 230 235 240		
Asn Pro Thr Gly Asp Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe 245 250 255		
Tyr Thr Val Ile Pro His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile 260 265 270		
Asn Ser Pro Asp Val Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu 275 280 285		
Ala Asp Ile Glu Leu Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu 290 295 300		
Glu Glu Lys Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln 305 310 315 320		
Leu Leu Arg Cys Gln Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr 325 330 335		
Lys Ala Ile Gln Thr Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys 340 345 350		
Pro Asn Leu Arg His Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp 355 360 365		
Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His 370 375 380		
Gly Thr Asn Val Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg 385 390 395 400		
Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala 405 410 415		
Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly 420 425 430		
Gly His Gln Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys 435 440 445		
Glu His His Ile Thr Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro 450 455 460		
Gly Phe Asp Ser Val Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala 465 470 475 480		
Gln Asp Ile Glu Leu Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln 485 490 495		

Gly Pro Pro Val Gln Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln  
                   500                  505                  510

Ser Glu Tyr Leu Ile Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu  
           515                  520                  525

Leu Glu Ile His Leu  
       530

<210> 9  
 <211> 1587  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (1)...(1584)

<400> 9

atg gct cca aaa cga aag gcc tct gtg cag act gag ggc tcc aag aag           48  
 Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys  
       1                  5                  10                  15

cag cga caa ggg aca gag gag gag gac agc ttc cgg tcc act gcc gag           96  
 Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu  
           20                  25                  30

gct ctc aga gca gca cct gct gat aat cgg gtc atc cgt gtg gac ccc           144  
 Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro  
           35                  40                  45

tca tgt cca ttc agc cgg aac ccc ggg ata cag gtc cac gag gac tat           192  
 Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr  
           50                  55                  60

gac tgt acc ctg aac cag acc aac atc ggc aac aac aac aac aag ttc           240  
 Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe  
       65                  70                  75                  80

tat att atc caa ctg ctg gag gag ggt agt cgc ttc ttc tgc tgg aat           288  
 Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn  
           85                  90                  95

~~cgc tgg ggc cgc gtg gga gag gtg ggc cag agc aag atg aac cac ttc           336~~  
~~Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe~~  
~~100                  105                  110~~

acc tgc ctg gaa gat gca aag aag gac ttt aag aag aaa ttt tgg gag           384  
 Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu  
       115                  120                  125

aag act aaa aac aaa tgg gag gag cgg gac cgt ttt gtg gcc cag ccc	432
Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro	
130 135 140	
aac aag tac aca ctt ata gaa gtc cag gga gaa gca gag agc caa gag	480
Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu	
145 150 155 160	
gct gta gtg aag gtg gac agc ggc cct gtg agg acc gtg gtc aag ccc	528
Ala Val Val Lys Val Asp Ser Gly Pro Val Arg Thr Val Val Lys Pro	
165 170 175	
tgc tcc cta gac cct gcc acc cag aac ctt atc acc aac atc ttc agc	576
Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn Ile Phe Ser	
180 185 190	
aaa gag atg ttc aag aac gca atg acc ctc atg aac ctg gat gtg aag	624
Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu Asp Val Lys	
195 200 205	
aag atg ccc ttg gga aag ctg acc aag cag cag att gcc cgt ggc ttc	672
Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala Arg Gly Phe	
210 215 220	
gag gcc ttg gaa gct cta gag gag gcc atg aaa aac ccc aca ggg gat	720
Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro Thr Gly Asp	
225 230 235 240	
ggc cag agc ctg gaa gag ctc tcc tcc tgc ttc tac act gtc atc cca	768
Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr Val Ile Pro	
245 250 255	
cac aac ttc ggc cgc agc cga ccc ccg ccc atc aac tcc cct gat gtg	816
His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser Pro Asp Val	
260 265 270	
ctt cag gcc aag aag gac atg ctg ctg gtg cta gcg gac atc gag ttg	864
Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu	
275 280 285	
gcg cag acc ttg cag gca gcc cct ggg gag gag gag gag aaa gtg gaa	912
Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Glu Lys Val Glu	
290 295 300	
<del>gag gtg cca cac cca ctg gat cga gac tac cag ctc ctc agg tgc cag</del>	<del>960</del>
<del>Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu Arg Cys Gln</del>	
<del>305 310 315 320</del>	
ctt caa ctg ctg gac tcc ggg gag tcc gag tac aag gca ata cag acc	1008
Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala Ile Gln Thr	
325 330 335	
tac ctg aaa cag act ggc aac agc tac agg tgc cca aac ctg cgg cat	1056



Tyr	Leu	Lys	Gln	Thr	Gly	Asn	Ser	Tyr	Arg	Cys	Pro	Asn	Leu	Arg	His	
			340					345					350			
gtt	tgg	aaa	gtg	aac	cga	gaa	ggg	gag	gga	gac	agg	ttc	cag	gcc	cac	1104
Val	Trp	Lys	Val	Asn	Arg	Glu	Gly	Glu	Gly	Asp	Arg	Phe	Gln	Ala	His	
		355					360					365				
tcc	aaa	ctg	ggc	aat	cgg	agg	ctg	ctg	tgg	cac	ggc	acc	aat	gtg	gcc	1152
Ser	Lys	Leu	Gly	Asn	Arg	Arg	Leu	Leu	Trp	His	Gly	Thr	Asn	Val	Ala	
		370					375				380					
gtg	gtg	gct	gcc	atc	ctc	acc	agt	ggg	ctc	cga	atc	atg	cca	cac	tcg	1200
Val	Val	Ala	Ala	Ile	Leu	Thr	Ser	Gly	Leu	Arg	Ile	Met	Pro	His	Ser	
		385				390				395					400	
ggg	ggg	cgt	gtt	ggc	aag	ggg	att	tat	ttt	gcc	tct	gag	aac	agc	aag	1248
Gly	Gly	Arg	Val	Gly	Lys	Gly	Ile	Tyr	Phe	Ala	Ser	Glu	Asn	Ser	Lys	
				405					410					415		
tca	gct	ggc	tat	gtt	acc	acc	atg	cac	tgt	ggg	ggc	cac	cag	gtg	ggc	1296
Ser	Ala	Gly	Tyr	Val	Thr	Thr	Met	His	Cys	Gly	Gly	His	Gln	Val	Gly	
			420					425					430			
tac	atg	ttc	ctg	ggc	gag	gtg	gcc	ctc	ggc	aaa	gag	cac	cac	atc	acc	1344
Tyr	Met	Phe	Leu	Gly	Glu	Val	Ala	Leu	Gly	Lys	Glu	His	His	Ile	Thr	
		435					440				445					
atc	gat	gac	ccc	agc	ttg	aag	agt	cca	ccc	cct	ggc	ttt	gac	agc	gtc	1392
Ile	Asp	Asp	Pro	Ser	Leu	Lys	Ser	Pro	Pro	Pro	Gly	Phe	Asp	Ser	Val	
		450				455					460					
atc	gcc	cga	ggc	caa	acc	gag	ccg	gat	ccc	gcc	cag	gac	att	gaa	ctt	1440
Ile	Ala	Arg	Gly	Gln	Thr	Glu	Pro	Asp	Pro	Ala	Gln	Asp	Ile	Glu	Leu	
		465				470				475					480	
gaa	ctg	gat	ggg	cag	ccg	gtg	gtg	gtg	ccc	caa	ggc	ccg	cct	gtg	cag	1488
Glu	Leu	Asp	Gly	Gln	Pro	Val	Val	Val	Pro	Gln	Gly	Pro	Pro	Val	Gln	
			485						490				495			
tgc	ccg	tca	ttc	aaa	agc	tcc	agc	ttc	agc	cag	agt	gaa	tac	ctc	ata	1536
Cys	Pro	Ser	Phe	Lys	Ser	Ser	Ser	Phe	Ser	Gln	Ser	Glu	Tyr	Leu	Ile	
			500					505					510			
tac	aag	gag	agc	cag	tgt	cgc	ctg	cgc	tac	ctg	ctg	gag	att	cac	ctc	1584
Tyr	Lys	Glu	Ser	Gln	Cys	Arg	Leu	Arg	Tyr	Leu	Leu	Glu	Ile	His	Leu	
		515					520					525				
taa																1587

<210> 10  
 <211> 528  
 <212> PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 10

Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys  
1 5 10 15

Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu  
20 25 30

Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro  
35 40 45

Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr  
50 55 60

Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe  
65 70 75 80

Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn  
85 90 95

Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe  
100 105 110

Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu  
115 120 125

Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro  
130 135 140

Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu  
145 150 155 160

Ala Val Val Lys Val Asp Ser Gly Pro Val Arg Thr Val Val Lys Pro  
165 170 175

Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn Ile Phe Ser  
180 185 190

Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu Asp Val Lys  
195 200 205

Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala Arg Gly Phe  
210 215 220

Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro Thr Gly Asp  
225 230 235 240

Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr Val Ile Pro  
245 250 255

His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser Pro Asp Val

260					265					270					
Leu	Gln	Ala	Lys	Lys	Asp	Met	Leu	Leu	Val	Leu	Ala	Asp	Il	Glu	Leu
	275						280					285			
Ala	Gln	Thr	Leu	Gln	Ala	Ala	Pro	Gly	Glu	Glu	Glu	Glu	Lys	Val	Glu
	290					295					300				
Glu	Val	Pro	His	Pro	Leu	Asp	Arg	Asp	Tyr	Gln	Leu	Leu	Arg	Cys	Gln
305					310					315					320
Leu	Gln	Leu	Leu	Asp	Ser	Gly	Glu	Ser	Glu	Tyr	Lys	Ala	Ile	Gln	Thr
				325					330					335	
Tyr	Leu	Lys	Gln	Thr	Gly	Asn	Ser	Tyr	Arg	Cys	Pro	Asn	Leu	Arg	His
			340					345					350		
Val	Trp	Lys	Val	Asn	Arg	Glu	Gly	Glu	Gly	Asp	Arg	Phe	Gln	Ala	His
	355						360					365			
Ser	Lys	Leu	Gly	Asn	Arg	Arg	Leu	Leu	Trp	His	Gly	Thr	Asn	Val	Ala
	370					375					380				
Val	Val	Ala	Ala	Ile	Leu	Thr	Ser	Gly	Leu	Arg	Ile	Met	Pro	His	Ser
385					390					395					400
Gly	Gly	Arg	Val	Gly	Lys	Gly	Ile	Tyr	Phe	Ala	Ser	Glu	Asn	Ser	Lys
				405					410					415	
Ser	Ala	Gly	Tyr	Val	Thr	Thr	Met	His	Cys	Gly	Gly	His	Gln	Val	Gly
		420						425					430		
Tyr	Met	Phe	Leu	Gly	Glu	Val	Ala	Leu	Gly	Lys	Glu	His	His	Ile	Thr
	435						440					445			
Ile	Asp	Asp	Pro	Ser	Leu	Lys	Ser	Pro	Pro	Pro	Gly	Phe	Asp	Ser	Val
	450					455					460				
Ile	Ala	Arg	Gly	Gln	Thr	Glu	Pro	Asp	Pro	Ala	Gln	Asp	Ile	Glu	Leu
465					470					475					480
Glu	Leu	Asp	Gly	Gln	Pro	Val	Val	Val	Pro	Gln	Gly	Pro	Pro	Val	Gln
				485					490					495	
Cys	Pro	Ser	Phe	Lys	Ser	Ser	Ser	Phe	Ser	Gln	Ser	Glu	Tyr	Leu	Ile
		500						505					510		
Tyr	Lys	Glu	Ser	Gln	Cys	Arg	Leu	Arg	Tyr	Leu	Leu	Glu	Ile	His	Leu
	515						520					525			

&lt;210&gt; 11

&lt;211&gt; 18

<212> PRT  
 <213> artificial sequence

<220>  
 <223> NAD+ binding domain

<220>  
 <221> VARIANT  
 <222> (2)...(6), (9)...(11)  
 <223> any amino acid; residues 3 to 6 may be present or absent

<220>  
 <221> VARIANT  
 <222> (7)  
 <223> amino acid residue 7 is either Ser or Thr

<400> 11

---

Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Gly	Lys	Gly	Ile	Tyr
1				5						10				15	

Phe Ala

<210> 12  
 <211> 25  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> NAD+ binding domain

<220>  
 <221> VARIANT  
 <222> (1), (14)  
 <223> amino acid residues 1 and 14 are either Ser or Thr

<220>  
 <221> VARIANT  
 <222> (2), (7), (9)...(13), (16)...(18)  
 <223> may be any amino acid; 10-13 may be present or absent

<220>  
 <221> VARIANT  
 <222> (6)  
 <223> amino acid residue 6 is either Ile or Val

---

<400> 12

Xaa	Xaa	Gly	Leu	Arg	Xaa	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Xaa
1				5						10				15	

Xaa Xaa Gly Lys Gly Ile Tyr Phe Ala

20

25

<210> 13  
 <211> 49  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> NAD+ binding domain

<220>  
 <221> VARIANT  
 <222> (6), (16), (29)  
 <223> Ser or Thr

<220>  
 <221> VARIANT  
 <222> (7)...(13), (17), (22), (24)...(28), (31)...(33), (41)...(43), (48)  
 <223> may be any amino acid; residues 25-28 may be present or absent

<220>  
 <221> VARIANT  
 <222> 21  
 <223> Ile or Val

<400> 13

Leu Leu Trp His Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Leu Xaa  
 1 5 10 15

Xaa Gly Leu Arg Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa  
 20 25 30

Xaa Gly Lys Gly Ile Tyr Phe Ala Xaa Xaa Xaa Ser Lys Ser Ala Xaa  
 35 40 45

Tyr

<210> 14  
 <211> 22  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> leucine zipper motif

<220>  
 <221> VARIANT  
 <222> (1)  
 <223> Leu or Val

<220>  
 <221> VARIANT  
 <222> (2)...(7), (9)...(14), (16)...(21)  
 <223> may be any amino acid

<400> 14

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa  
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Leu  
 20

<210> 15  
 <211> 37  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> part-sequence motif 1

<220>  
 <221> VARIANT  
 <222> (21)  
 <223> Asp or Glu

<220>  
 <221> VARIANT  
 <222> (2)...(10), (12)...(13), (15)...(16), (20), (22)...(32)  
 <223> may be any amino acid; residue 32 may be present or absent

<400> 15

Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Tyr Xaa Xaa  
 1 5 10 15

Gln Leu Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 20 25 30

Trp Gly Arg Val Gly  
 35

<210> 16  
 <211> 29  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> part-sequence motif 2

<220>

<221> VARIANT

<222> (2)...(4), (6), (8)...(11), (14), (16), (18)...(22), (24)...(26), (28)

<223> may be any amino acid

<400> 16

Ala Xaa Xaa Xaa Phe Xaa Lys Xaa Xaa Xaa Xaa Lys Thr Xaa Asn Xaa  
1 5 10 15

Trp Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Pro Xaa Lys  
20 25

<210> 17

<211> 44

<212> PRT

<213> artificial sequence

<220>

<223> part-sequence motif 3

<220>

<221> VARIANT

<222> (2), (5)...(6), (8)...(16), (18)...(27), (33)...(35), (38)...(43)

<223> may be any amino acid

<220>

<221> VARIANT

<222> (4)

<223> Ile or Leu

<400> 17

Gln Xaa Leu Xaa Xaa Xaa Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
1 5 10 15

Met Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Leu Gly Lys Leu  
20 25 30

Xaa Xaa Xaa Gln Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu  
35 40

<210> 18

<211> 15

<212> PRT

<213> artificial sequence

<220>

<223> part-sequence motif 4

<220>

<221> VARIANT

<222> (4), (8), (11)...(13)  
 <223> may be any amino acid

<400> 18

Phe	Tyr	Thr	Xaa	Ile	Pro	His	Xaa	Phe	Gly	Xaa	Xaa	Xaa	Pro	Pro
1				5					10				15	

<210> 19  
 <211> 17  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> part-sequence motif 5

<220>  
 <221> VARIANT  
 <222> (2)...(4), (6)...(7), (9), (13), (15)...(16)  
 <223> may be any amino acid

<400> 19

Lys	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Leu	Xaa	Asp	Ile	Glu	Xaa	Ala	Xaa	Xaa
1				5					10				15		

Leu

<210> 20  
 <211> 11  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> part-sequence motif 6

<220>  
 <221> VARIANT  
 <222> (2)...(4), (6)  
 <223> may be any amino acid

<400> 20

Gly	Xaa	Xaa	Xaa	Leu	Xaa	Glu	Val	Ala	Leu	Gly
1				5					10	

<210> 21  
 <211> 28



<212> PRT  
 <213> artificial sequence

<220>  
 <223> part-sequence motif 7

<220>  
 <221> VARIANT  
 <222> (2)...(3), (5)...(8), (10)...(12), (14)...(22), (24), (26)...(27)  
 <223> may be any amino acid; residues 21 and 22 may be present or absent

<400> 21

Gly Xaa Xaa Ser Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Pro Xaa Xaa Xaa  
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Gly Xaa Xaa Val  
 20 25

---

<210> 22  
 <211> 16  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> part-sequence motif 8

<220>  
 <221> VARIANT  
 <222> (2)  
 <223> Tyr or Phe

<220>  
 <221> VARIANT  
 <222> (3)...(4), (6)...(8), (10)...(13)  
 <223> may be any amino acid

<400> 22

Glu Xaa Xaa Xaa Tyr Xaa Xaa Xaa Gln Xaa Xaa Xaa Xaa Tyr Leu Leu  
 1 5 10 15

---

<210> 23  
 <211> 20  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> synthetic sequence for antibody production

<400> 23

Met Ala Ala Arg Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg Ala  
 1 5 10 15

Leu Asn Glu Ser  
 20

<210> 24  
 <211> 20  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> synthetic sequence for antibody production

<400> 24

Lys Thr Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg  
 1 5 10 15

Asn Leu His Cys  
 20

<210> 25  
 <211> 21  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> synthetic sequence for antibody production

<400> 25

Cys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser Thr  
 1 5 10 15

Ala Glu Ala Leu Lys  
 20

<210> 26  
 <211> 20  
 <212> PRT  
 <213> artificial sequence

<220>  
 <223> synthetic sequence for antibody production

<400> 26

Cys Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu  
 1 5 10 15

Glu Ala Leu Lys  
20

<210> 27  
<211> 19  
<212> PRT  
<213> artificial sequence

<220>  
<223> synthetic sequence for antibody production

<400> 27

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu  
1 5 10 15

Ala Leu Lys

---

<210> 28  
<211> 19  
<212> PRT  
<213> Mus musculus

<400> 28

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu  
1 5 10 15

Ala Met Lys

<210> 29  
<211> 7  
<212> PRT  
<213> artificial sequence

<220>  
<223> NAD+ binding domain

<220>  
<221> VARIANT  
<222> (2)...(4)  
<223> may be any amino acid residue

---

<400> 29

Gly Xaa Xaa Xaa Gly Lys Gly  
1 5

<210> 30

<211> 38  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> PARP zinc finger sequence motif

<220>  
 <221> VARIANT  
 <222> (2)...(3), (5)...(34), (36)...(37)  
 <223> may be any amino acid; residues 33 and 34 may be present or absent

<400> 30

Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 20 25 30

Xaa Xaa His Xaa Xaa Cys  
 35

<210> 31  
 <211> 10  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 31

Ala Ala Val Leu Asp Gln Trp Ile Pro Asp  
 1 5 10

<210> 32  
 <211> 39  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(39)

<400> 32

gta tgc cag gaa ggt cat ggg cca gca aaa ggg tct ctg  
 Gly Met Pro Gly Arg Ser Trp Ala Ser Lys Arg Val Ser  
 1 5 10

39

<210> 33  
 <211> 13

<212> PRT

<213> Homo sapiens

<400> 33

Gly Met Pro Gly Arg Ser Trp Ala Ser Lys Arg Val Ser  
1 5 10

---

---